

Figure 1

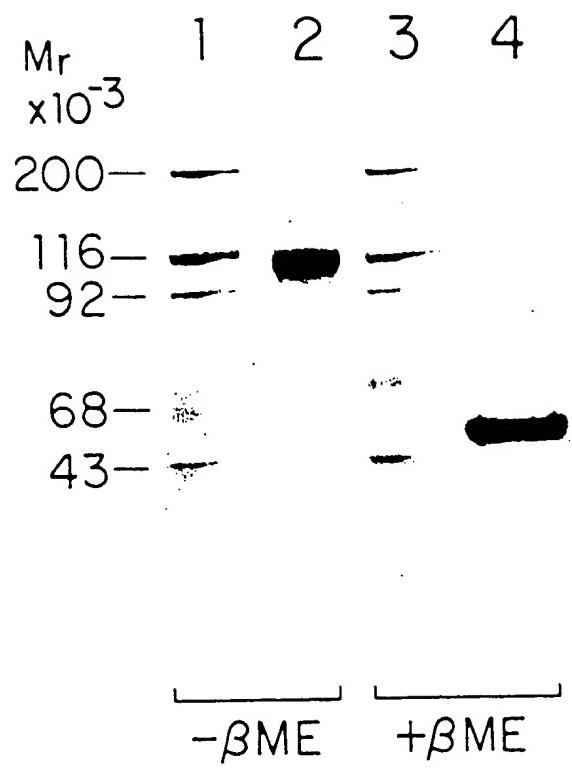


Figure 2

ONCOSTATIN M SIGNAL PEPTIDE

-25 -20
M G V L L T Q R T L L S L V L
ATG GGT GTA CTG CTC ACA CAG AGG ACG CTG CTC AGT CTG GTC CTT 45

-10 -1 +1

A	L	L	F	P	S	M	A	S	M	A	M	H	V	A
GCA	CTC	CTG	TTT	CCA	AGC	ATG	GCG	AGC	ATG	GCA	ATG	CAC	GTG	GCC

90

Q	P	A	V	+10	V	L	A	S	S	R	G	I	A	S	+20	F	
CAG	CCT	GCT	GTG		GTA	CTG	GCC	AGC	AGC	CGA	GGC	ATC	GCC	AGC	TTT		135

V	C	E	Y	A	S	P	G	K	A	T	E	V	R	V	+30		180
GTG	TGT	GAG	TAT	GCA	TCT	CCA	GGC	AAA	GCC	ACT	GAG	GTC	CGG	GTG			

+40																	+50
T	V	L	R	Q	A	D	S	Q	V	T	E	V	C		A		
ACA	GTG	CTT	CGG	CAG	GCT	GAC	AGC	CAG	GTG	ACT	GAA	GTC	TGT	GCG			

A	T	Y	M	M	G	N	E	L	+60	T	F	L	D	D	S
GCA	ACC	TAC	ATG	ATG	GGG	AAT	GAG	TTG	ACC	TTC	CTA	GAT	GAT	TCC	

+70		+80
I C T G T S S G N Q V N L T T I		
ATC TGC ACG GGC ACC TCC AGT CGA AAT CAA GTG AAC CTC ACT ATC		315

Q	G	L	R	A	M	D	T	G	L	Y	I	C	K	V	+90
CAA	GGA	CTG	AGG	GCC	ATG	GAC	ACG	GGA	CTC	TAC	ATC	TGC	AAG	GTG	360

GLYCOSYLATION SITE

+100	+110
E L M Y P P P Y Y L G I G N G	GAG CTC ATG TAC CCA CCG CCA TAC TAC CTG GGC ATA GGC AAC GGA
	405

+120

T	Q	I	Y	V	I	D	P	E	P	C	P	D	S	D	
ACC	CAG	ATT	TAT	GTA	ATT	GAT	CCA	GAA	CCG	TGC	CCA	GAT	TCT	GAC	450

F	L	L	W	I	L	A	A	V	S	S	G	L	F	F	+130	
TTC	CTC	CTC	TGG	ATC	CTT	GCA	GCA	GTT	AGT	TCG	GGG	TTG	TTT	TTT		495

+140	+150
Y S F L L T A V S L S K M L K	
TAT AGC TTT CTC CTC ACA GCT GTT TCT TTG AGC AAA ATG CTA AAG	540

K	R	S	P	L	T	T	G	V	Y	V	K	M	P	P	+160
AAA	AGA	AGC	CCT	CTT	ACA	ACA	GGG	GTC	TAT	GTG	AAA	ATG	CCC	CCA	585

+170	+180
T E P E C K Q F Q P Y F I P	
ACA GAG CCA GAA TGT GAA AAG CAA TTT CAG CCT TAT TTT ATT CCC	
	630

I +187
N
ATC AAT 636

Figure 3

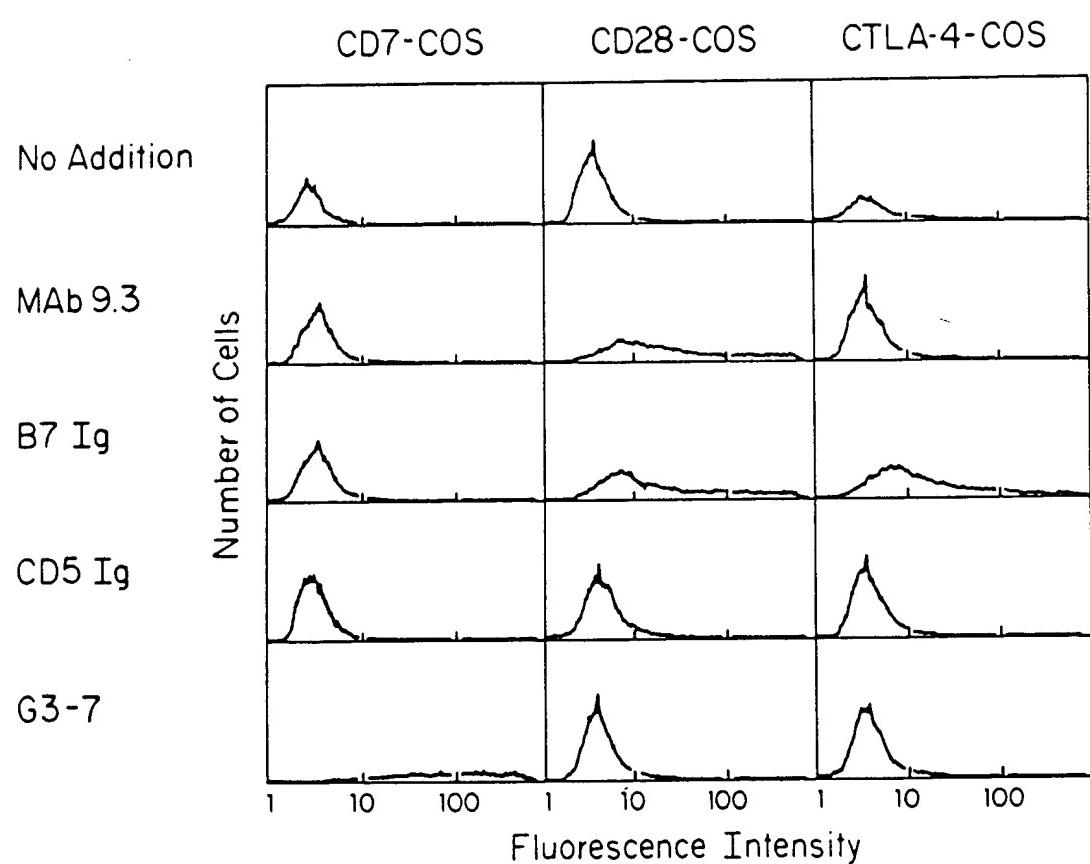


Figure 4

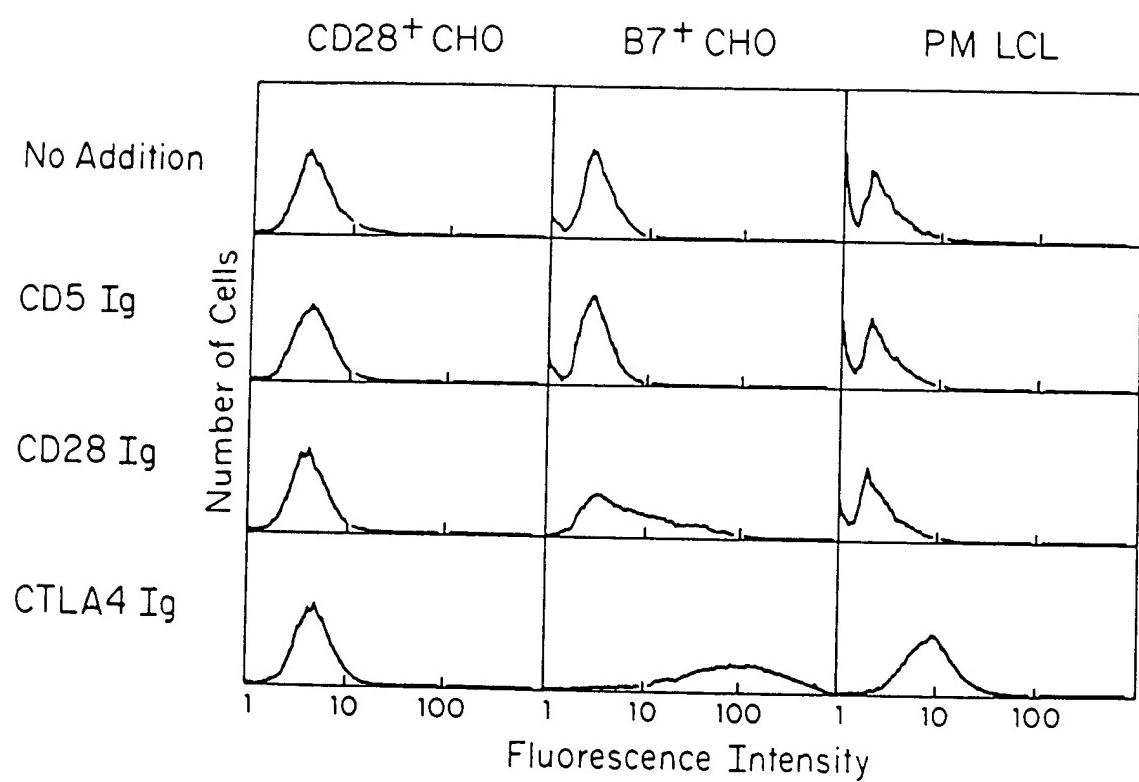


Figure 5

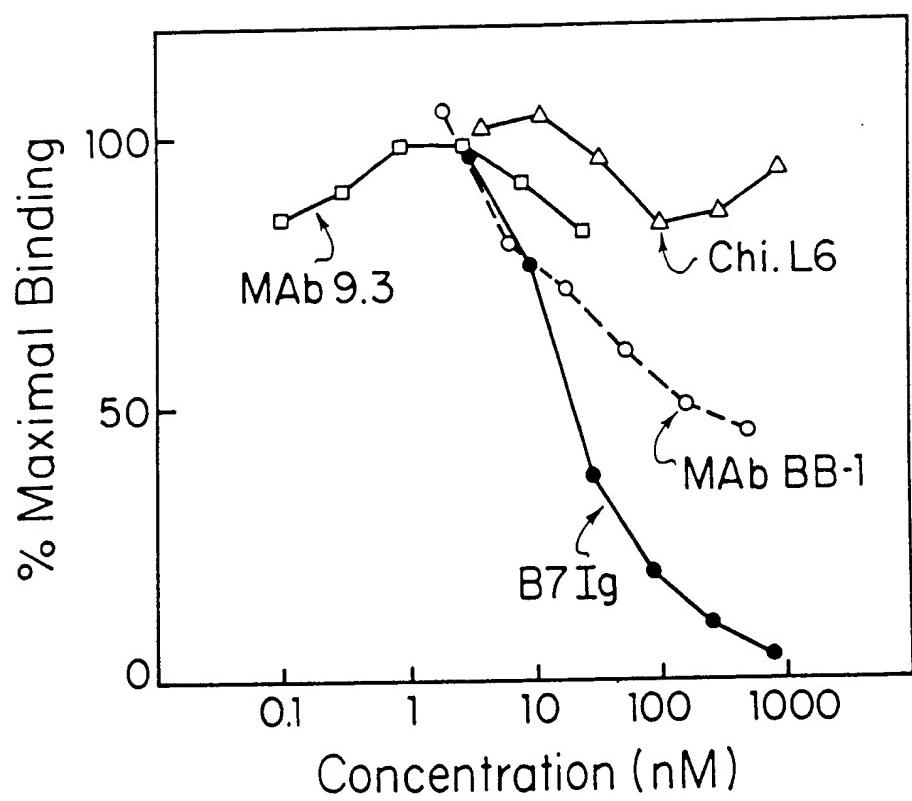


Figure 6

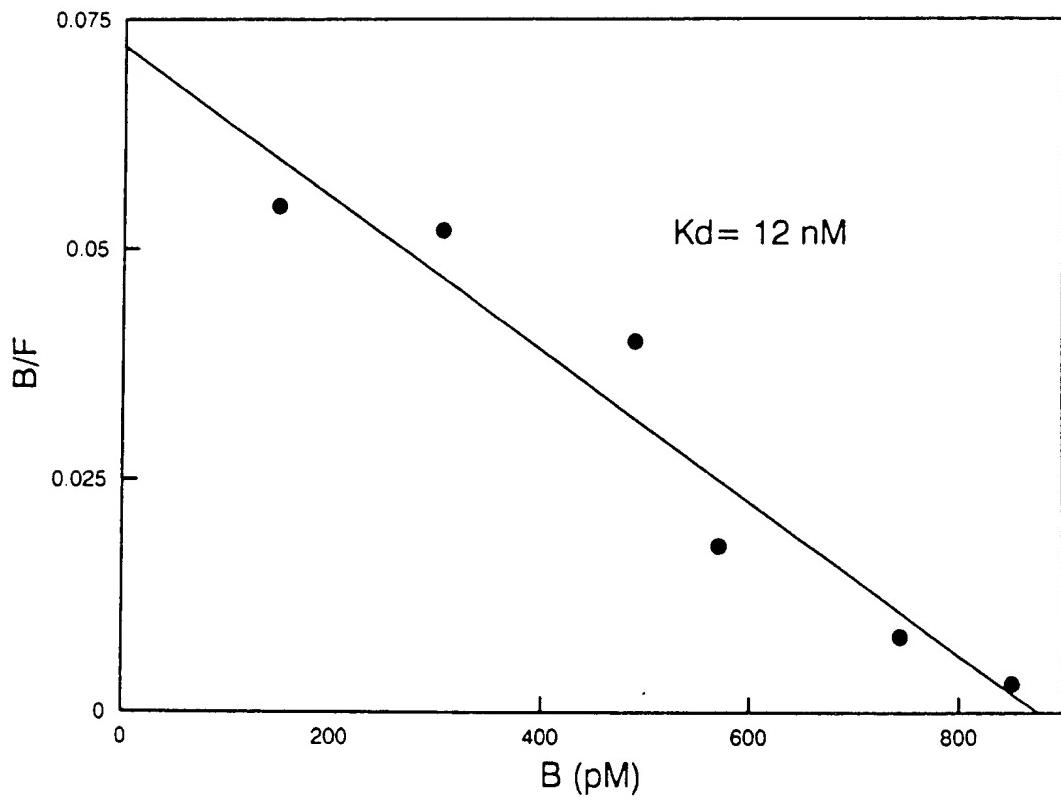


Figure 7

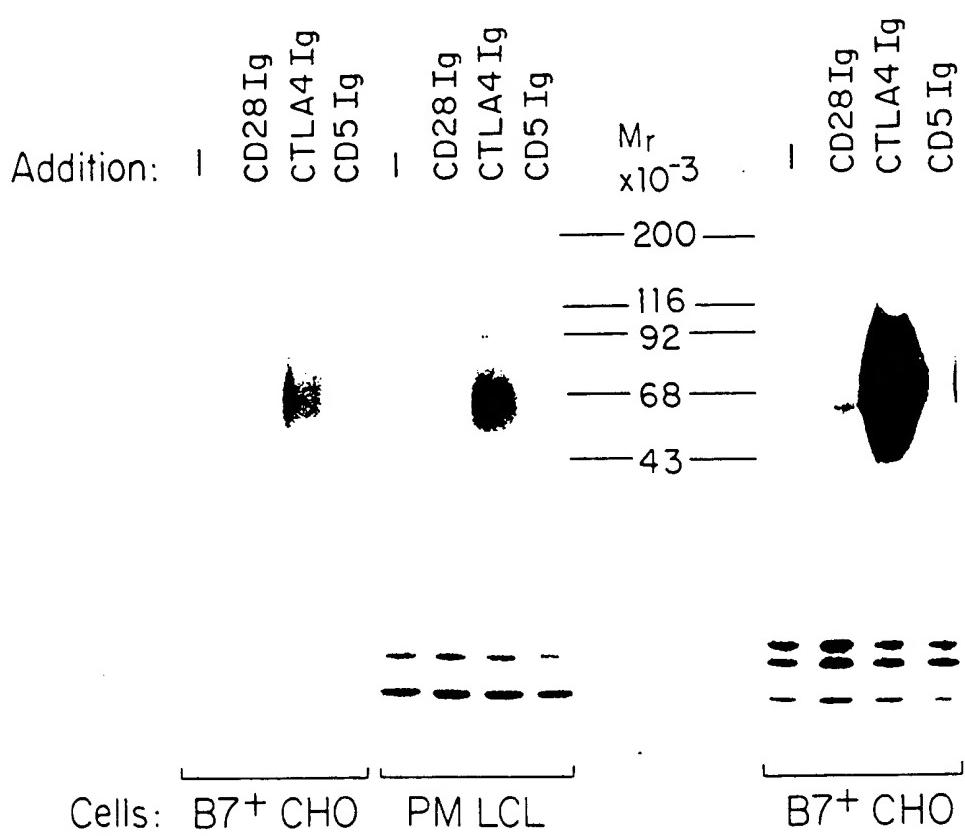


Figure 8

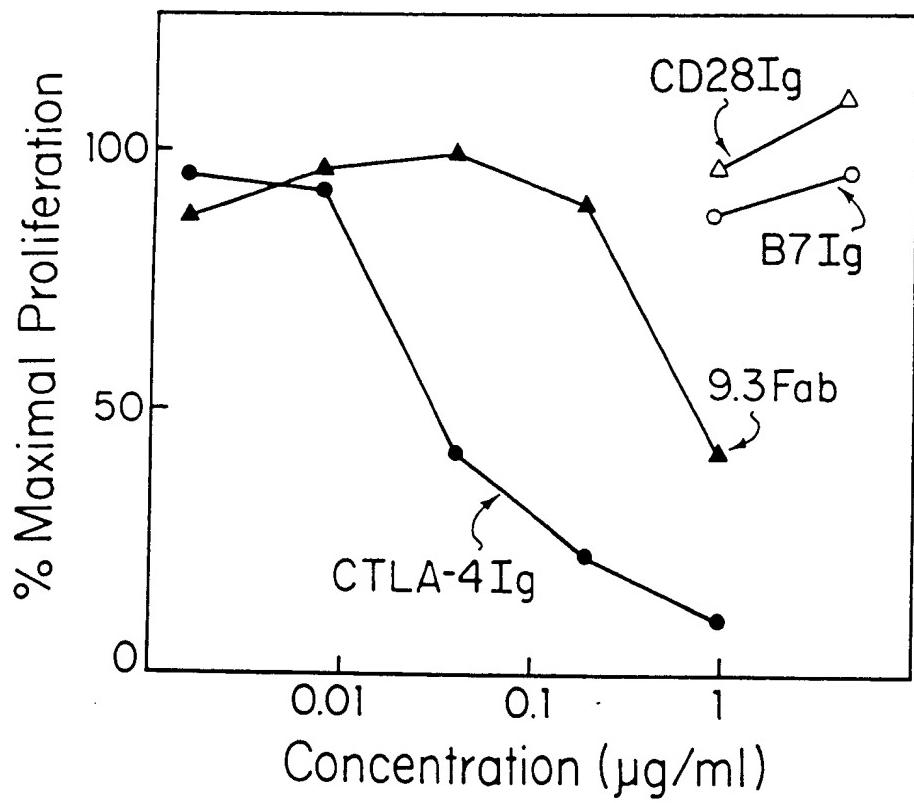


Figure 9

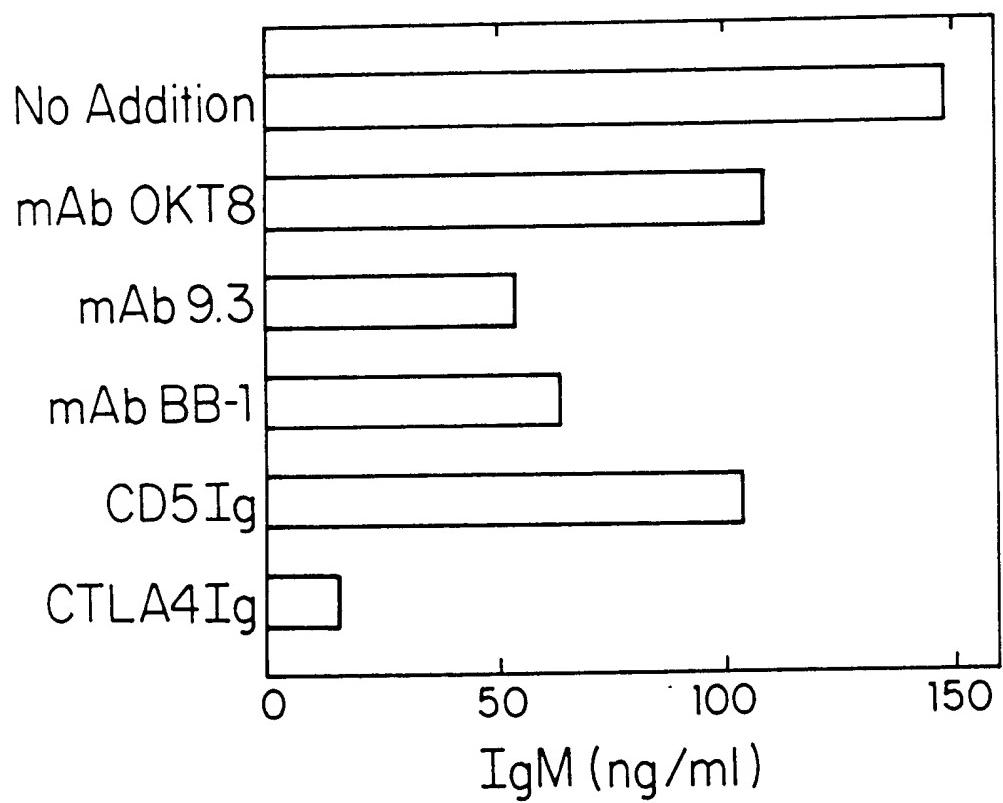


Figure 10

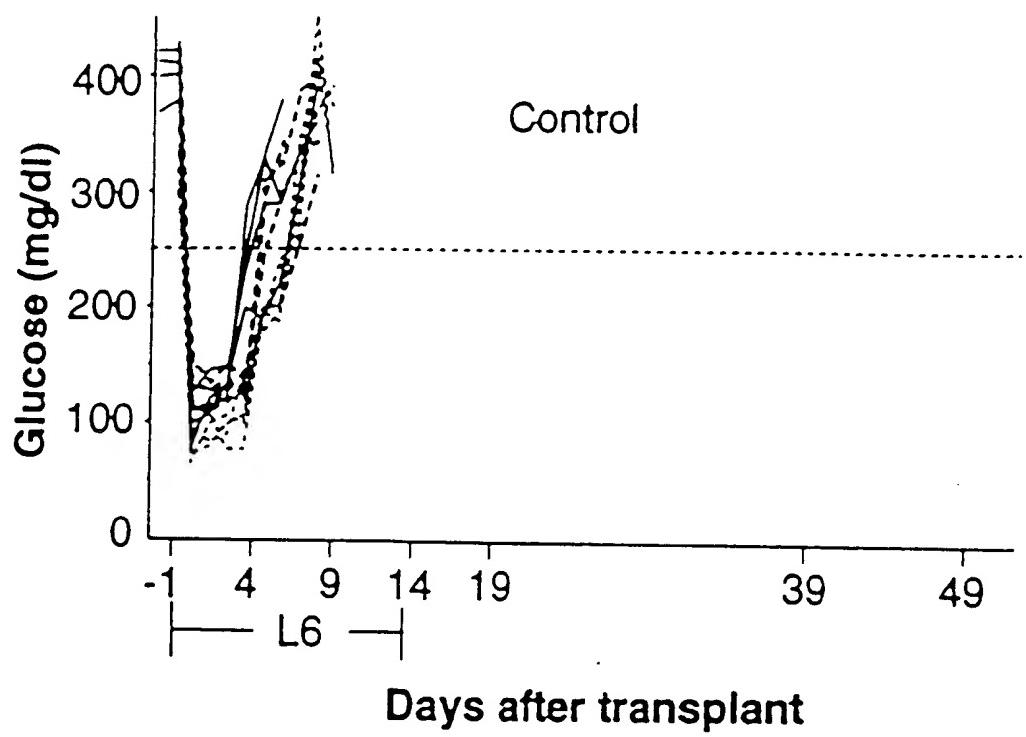


Figure 11A

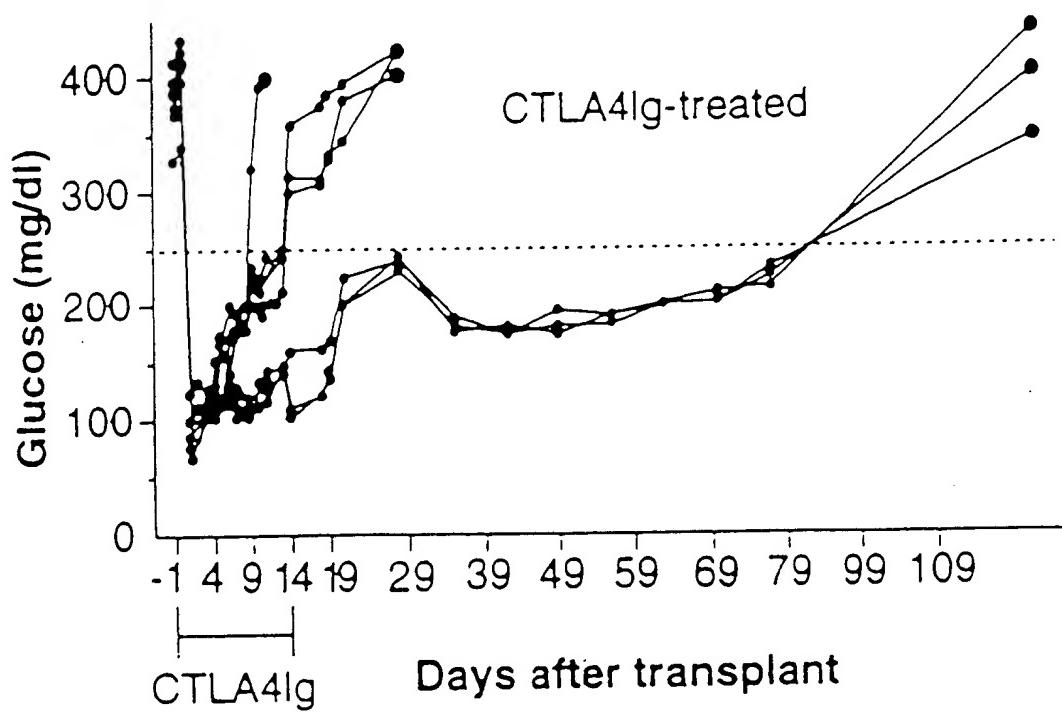


Figure 11B

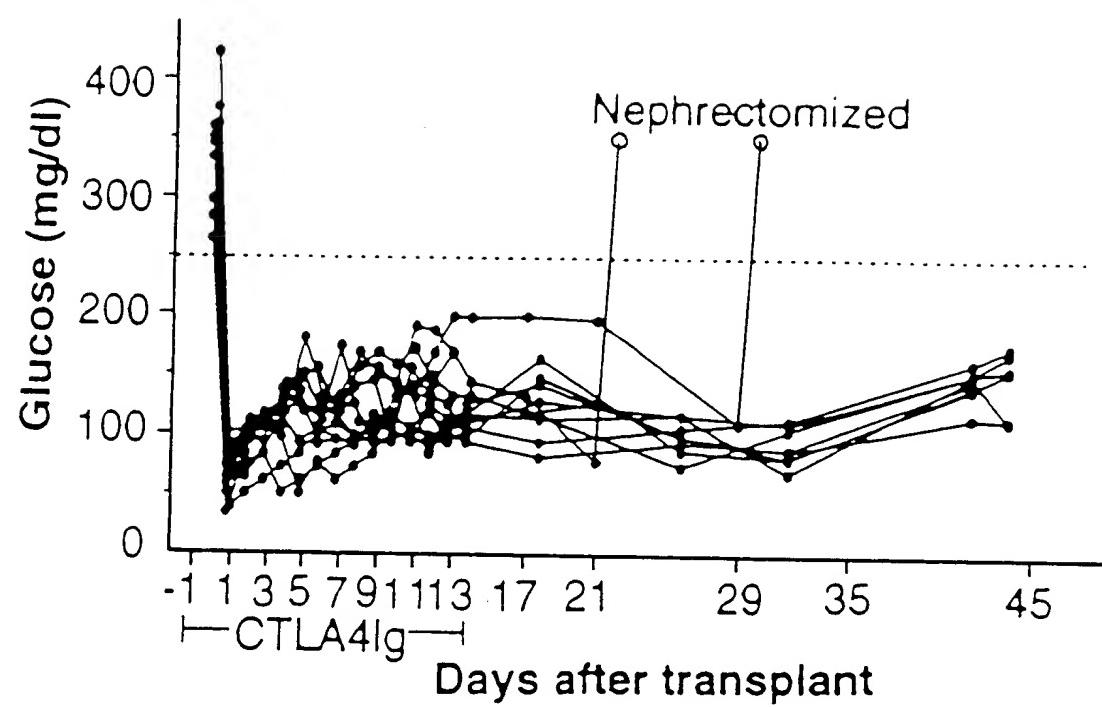


Figure 11C

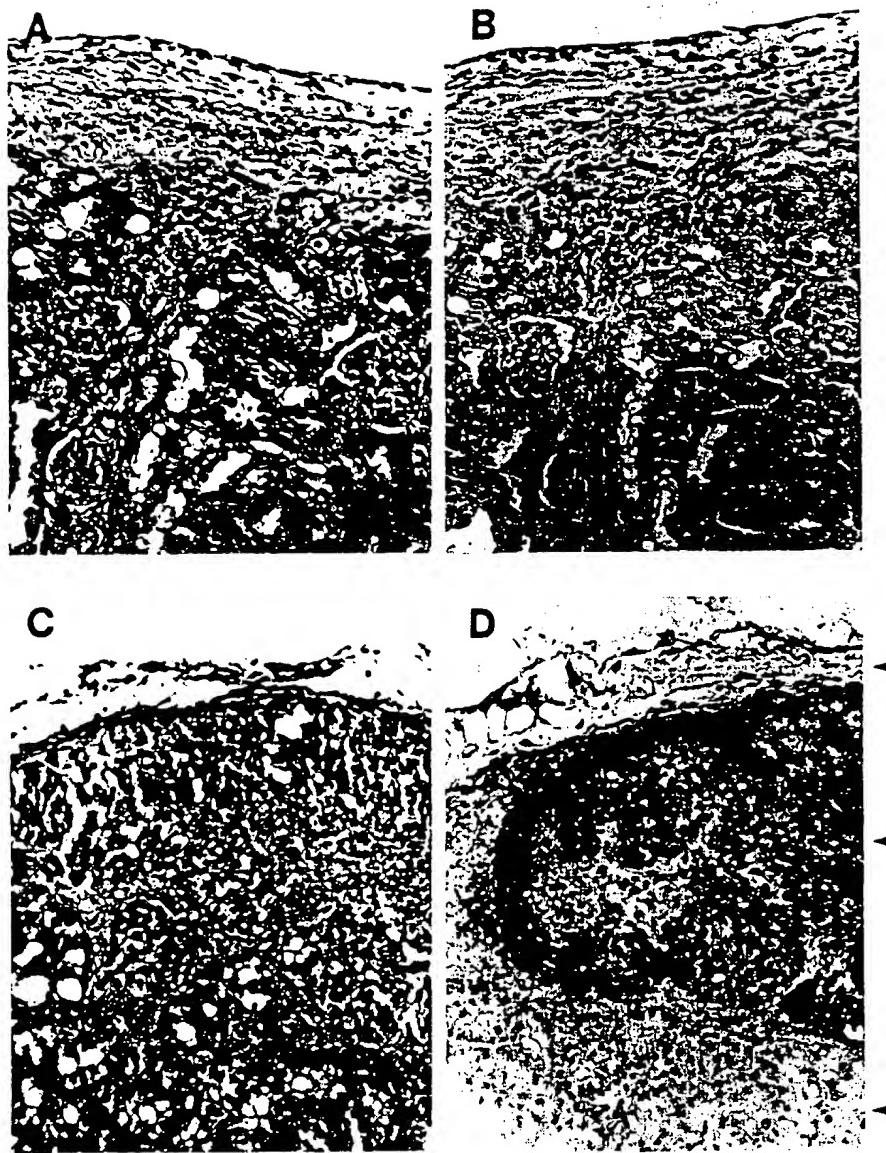


Figure 12

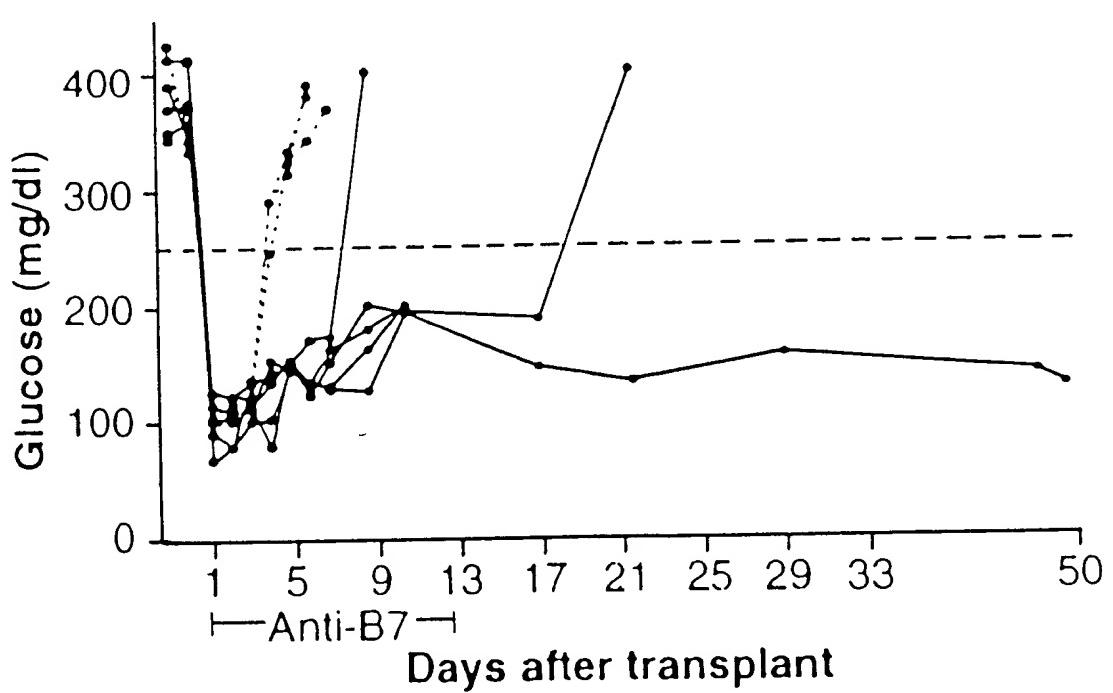


Figure 13

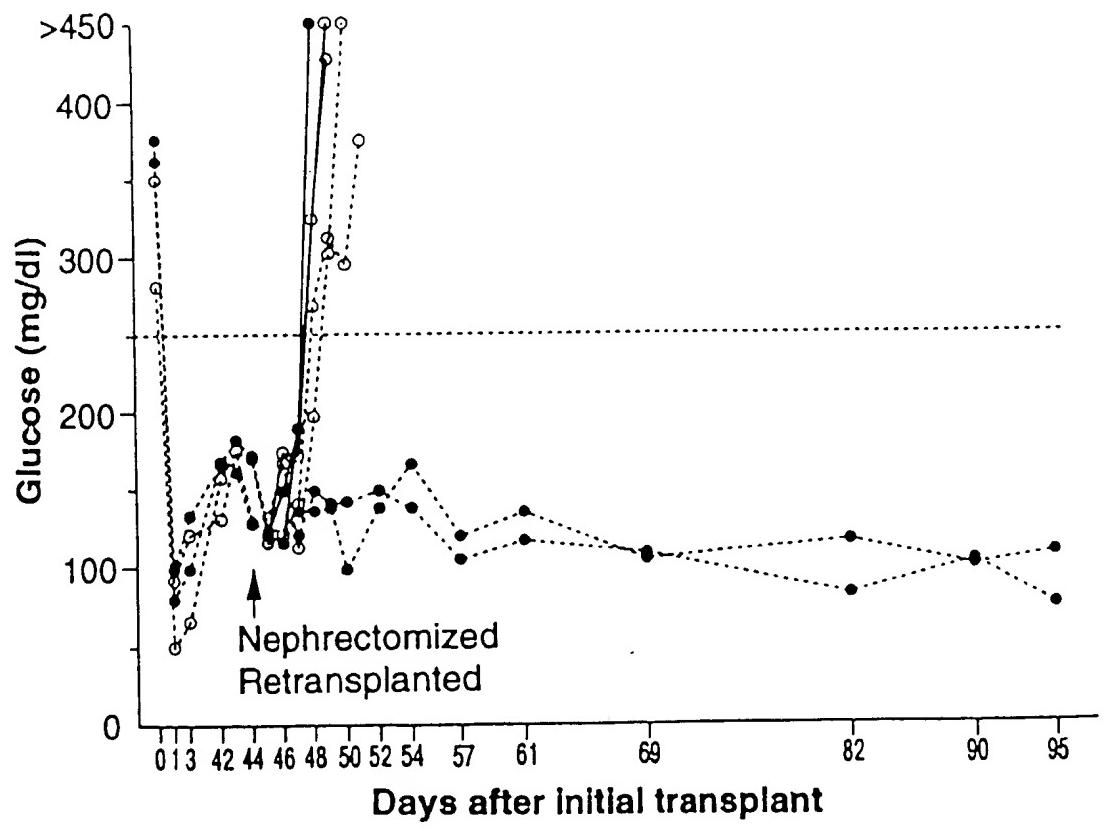


Figure 14

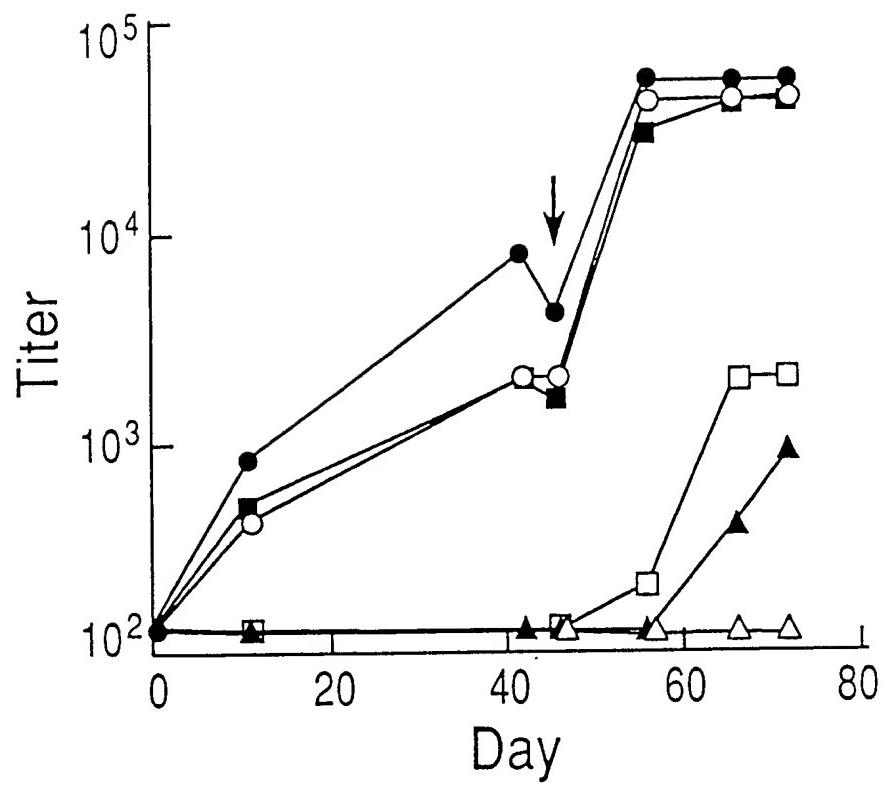


Figure 15

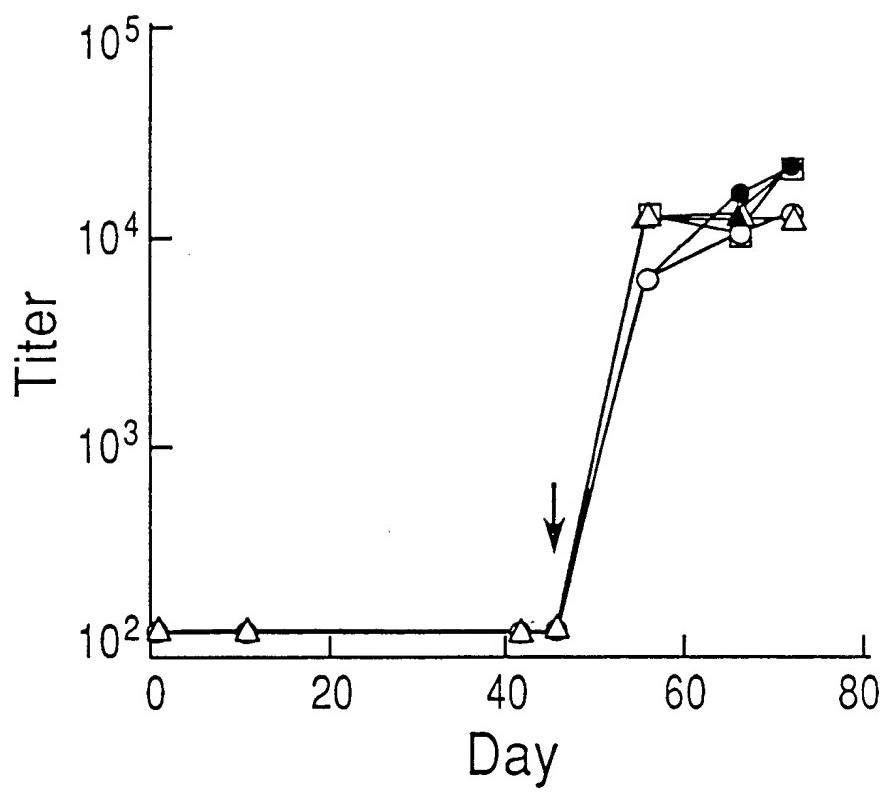


Figure 16

FIGURE 17

CD28/CTLA-4 family

The figure displays a sequence alignment of six proteins (Hctla4, Muclta4, Ncd28, Rcd28, Hcd28, Chcd28) across three domains: CDR1-like, transmembrane domain, and CDR2-like. The alignment is color-coded by residue type and includes a signal peptide at the top.

CDR1-like: Positions 51 to 101. The alignment shows highly conserved regions, particularly in the first half (residues 51-75), where many amino acids are identical across all proteins. The second half (residues 76-101) shows more variation, with Hctla4 and Muclta4 diverging from the others.

transmembrane domain: Positions 101 to 200. This domain is characterized by a high density of hydrophobic residues (black squares). The alignment highlights a conserved hydrophobic cluster in the center of the domain.

CDR2-like: Positions 200 to 1000. This domain contains several stretches of conserved polar residues (shaded squares) interspersed with hydrophobic regions. The alignment shows significant divergence between Hctla4/Muclta4 and the other four proteins in this domain.

FIGURE 18

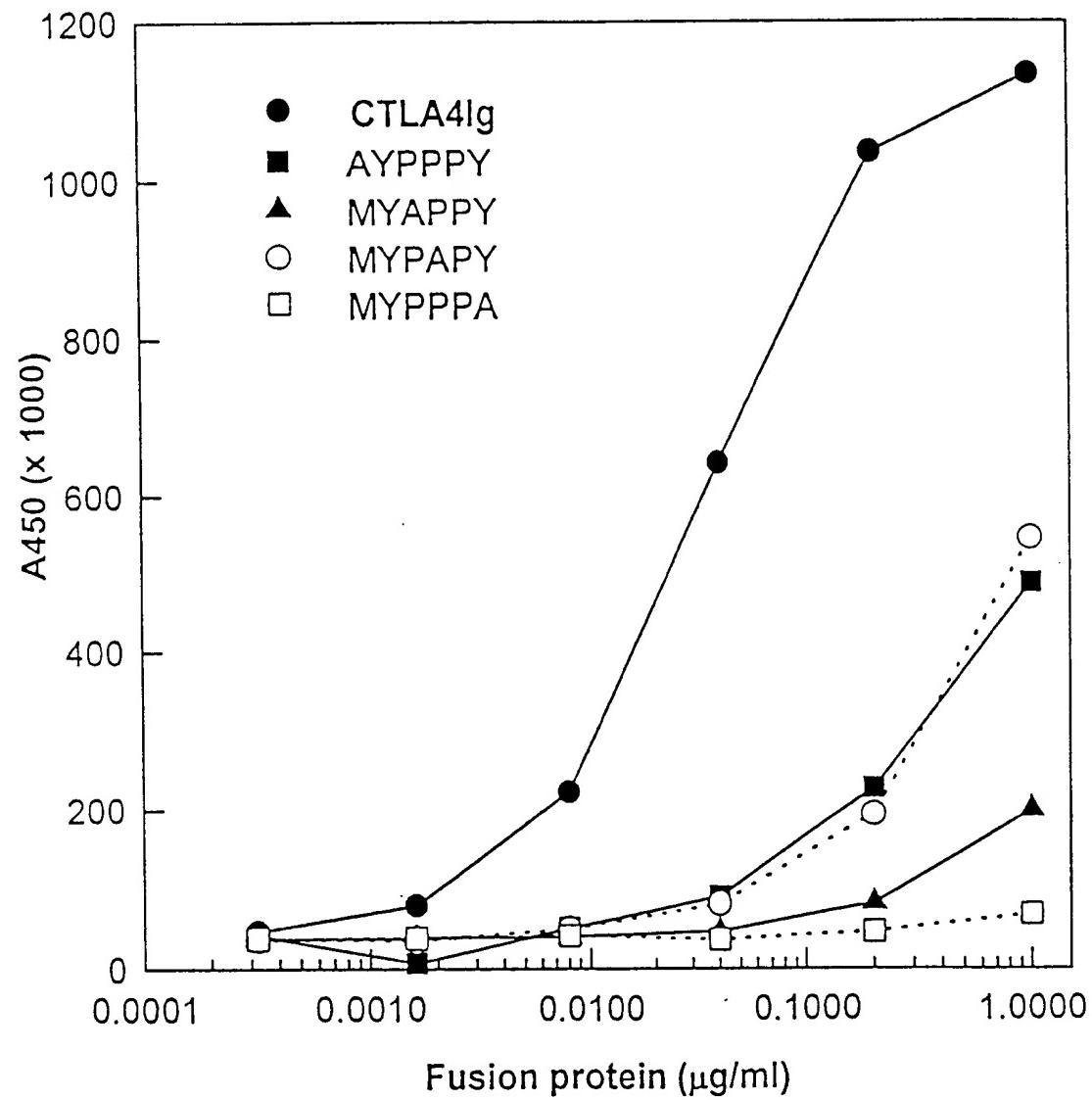


FIGURE 19

*% B7
Binding Activity*

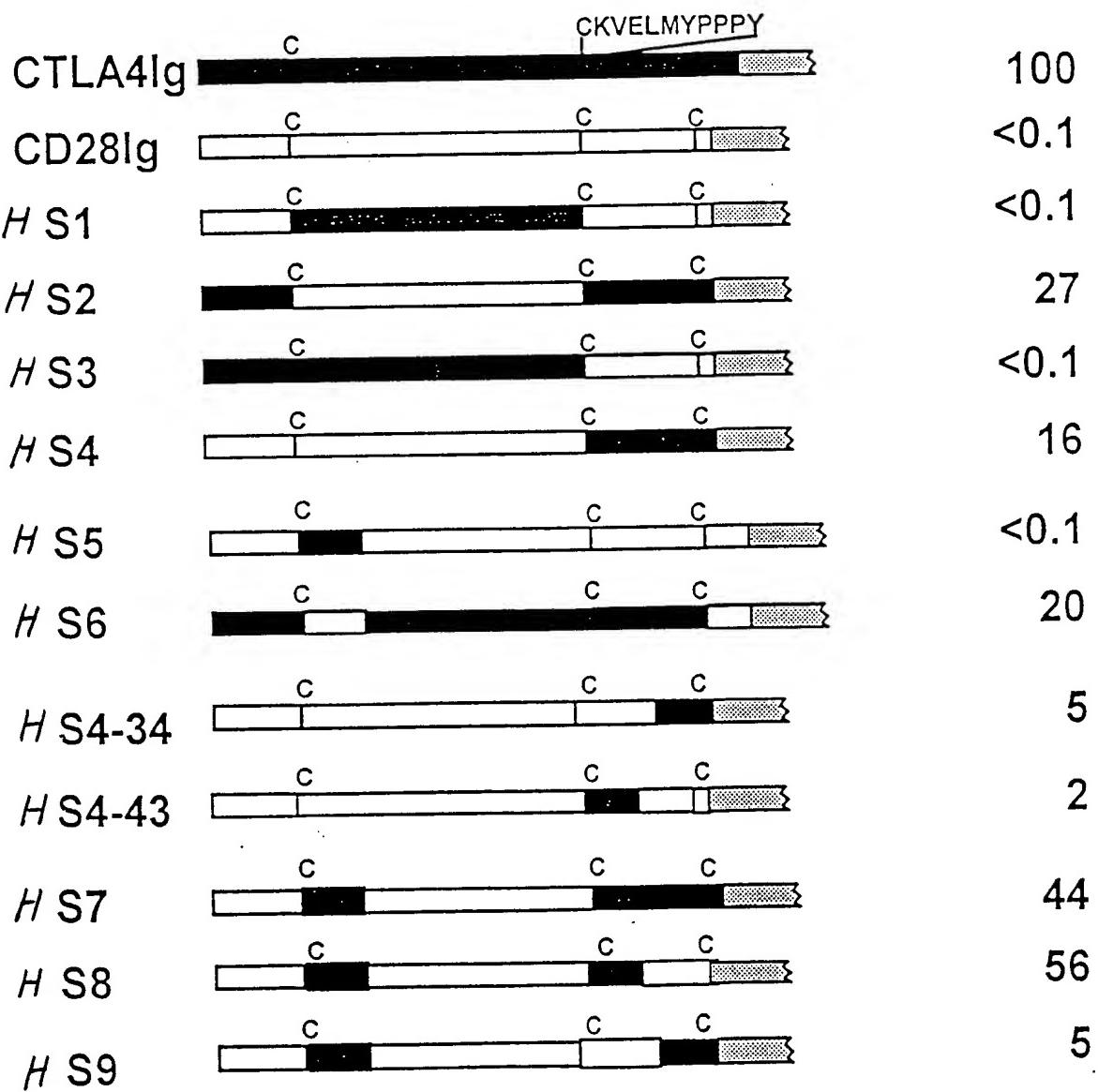


FIGURE 20(a)

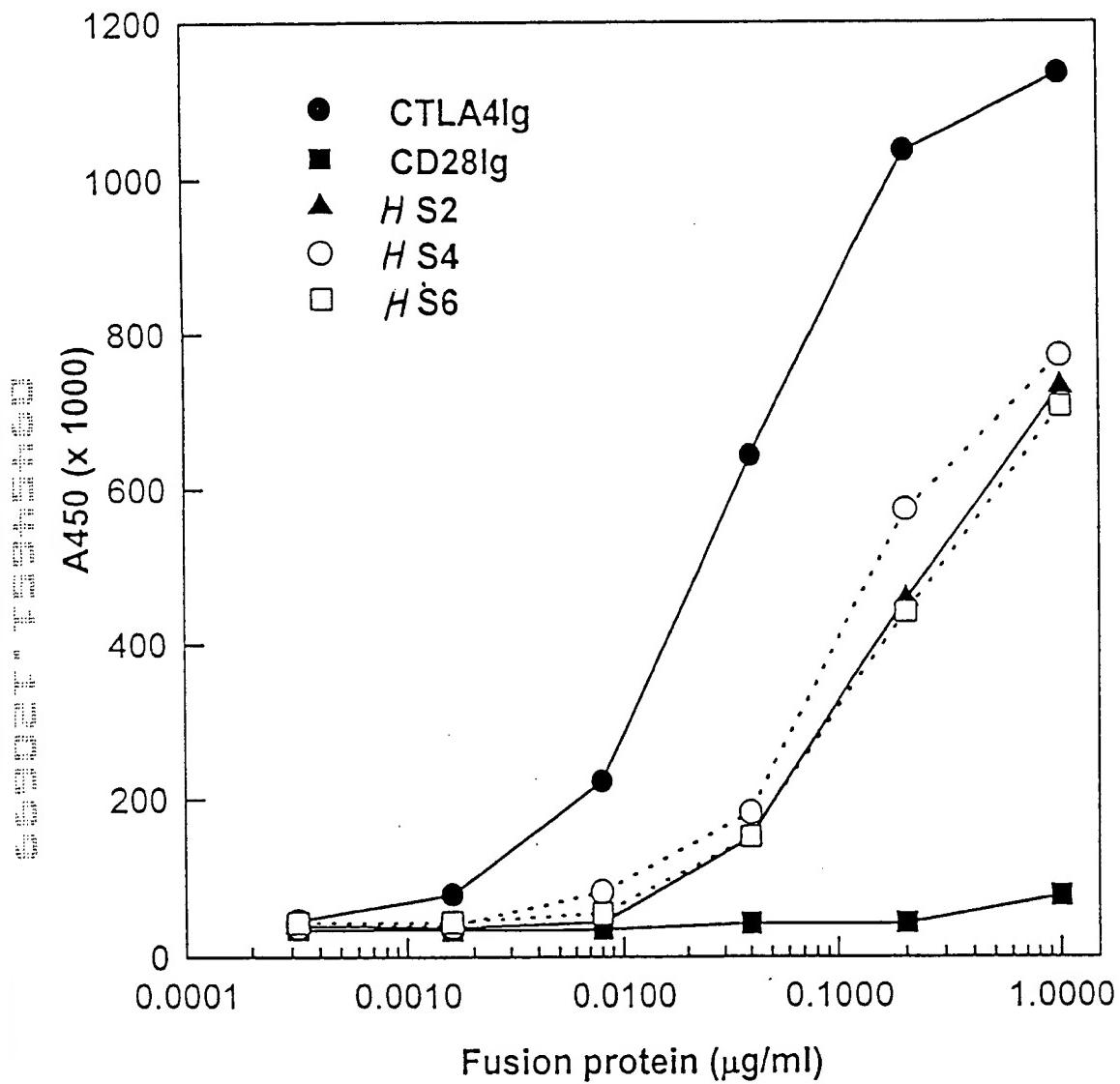


FIGURE 20(b)

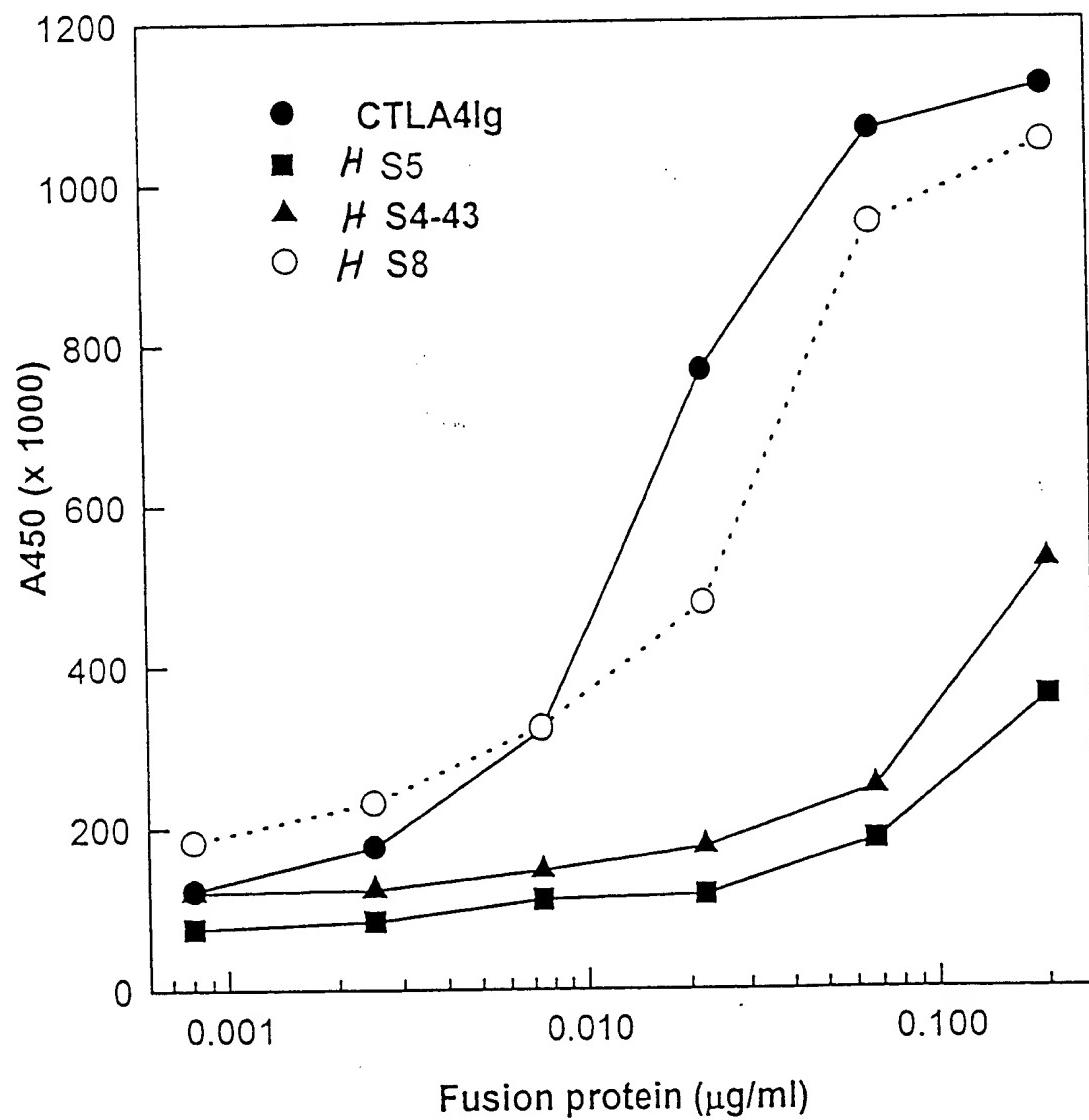


FIGURE 21

